

**INFORMATION DISCLOSURE
STATEMENT BY APPLICANT**
(Not for submission under 37 CFR 1.99)

Application Number	10588685
Filing Date	2007-06-21
First Named Inventor	Fabian Model
Art Unit	1797
Examiner Name	Unassigned
Attorney Docket Number	7003/54

MAY 27 2008

U.S.PATENTS						
Examiner Initial*	Cite No	Patent Number	Kind Code ¹	Issue Date	Name of Patentee or Applicant of cited Document	Pages, Columns, Lines where Relevant Passages or Relevant Figures Appear
	1	6331393	B1	2001-12-18	Laird et al.	
	2	6124120		2000-09-26	Lizardi	
	3	6280949	B1	2001-08-28	Lizardi	
	4	6642034	B2	2003-11-04	Lizardi	

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U.S.PATENT APPLICATION PUBLICATIONS

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	1	20030082600	A1	2003-05-01	Alexander et al.	
	2	20030143536	A1	2003-07-31	Lizardi	

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	3	20040115663	A1	2004-06-17	Berlin et al.	
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FOREIGN PATENT DOCUMENTS

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	1	2004051224	WO	A3	2004-06-17	Illumina, Inc.		<input type="checkbox"/>
	2	03085132	WO	A2	2003-10-16	Epigenomics AG		<input type="checkbox"/>
	3	0183796	WO	A2	2001-11-08	University of Washington		<input type="checkbox"/>
	4	02072880	WO	A2	2002-09-19	Epigenomics AG (English abstract included)		<input checked="" type="checkbox"/>
	5	0070090	WO	A1	2000-11-23	University Southern California		<input type="checkbox"/>
	6	101 54 317	DE	A1	2003-05-15	Epigenomics AG (English abstract included)		<input checked="" type="checkbox"/>
	7	101 12 515	DE	A1	2002-11-14	Epigenomics AG (English Abstract included)		<input checked="" type="checkbox"/>
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NON-PATENT LITERATURE DOCUMENTS

Examiner Initials*	Cite No	Include name of the author (in CAPITAL LETTERS), title of the article (when appropriate), title of the item (book, magazine, journal, serial, symposium, catalog, etc), date, pages(s), volume-issue number(s), publisher, city and/or country where published.	T5
	1	DEAN, F.B. et al., "Comprehensive human genome amplification using multiple displacement amplification", Proceedings of the National Academy of Sciences of USA, National Academy of Science, Washington, US, Vol. 99, No. 8, 16 April 2002, pp. 5261-5266.	<input type="checkbox"/>
	2	MILLAR, L. et al, "Five Not Four: History and Significance of the Fifth Base", The Epigenome: Molecular Hide and Seek, S Beck et al. editors, Wiley-VCH, 2003, pp. 3-20.	<input type="checkbox"/>
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	5	TRINH, B.N. et al., "DNA Methylation Analysis by MethylLight Technology", Methods 25, 2001, pp. 456-462.	<input type="checkbox"/>
	6	HAWKINS, T.L. et al., "Whole genome amplification-applications and advances", Curr Opin Biotechnol, 2002, 13, pp. 65-67.	<input type="checkbox"/>
	7	ZHANG, L. et al., "Whole genome amplification from a single cell: Implications for genetic analysis", Proc Natl Acad Sci USA, July 1, 1992, Vol. 89, pp. 5847-5851.	<input type="checkbox"/>
	8	TELENIUS, H. et al., Degenerate Oligonucleotide-Primed PCR: General Amplification of Target DNA by a Single Degenerate Primer", Genomics 13, 1992, pp. 718-725.	<input type="checkbox"/>
	9	CHEUNG, V.G et al., "Whole genome amplification using a degenerate oligonucleotide primer allows hundreds of genotypes to be performed on less than one nanogram of genomic DNA", Proc Natl Acad Sci USA, 1996 Dec 10; Vol. 93(25): 14676-9.	<input type="checkbox"/>

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	10	www.4amershambiosciences.com, GenomiPhi DNA Amplification Kit, 28 pp., copyright 2003.	<input type="checkbox"/>
	11	QIAamp DNA Mini Kit and QIAamp Blood Mini Kit Handbook, Feb. 2003, 68 pp.	<input type="checkbox"/>
	12	GONZALGO, M. L. et al., "Rapid quantitation of methylation differences at specific sites using methylation-sensitive single nucleotide primer extension(Ms- SNuPE)", Nucleic Acids Res., Jun 15, 1997, Vol. 25, No. 12, pp. 2529-2531.	<input type="checkbox"/>
	13	ADORJAN, P. et al., "Tumor class prediction and discovery by microarray-based DNA methylation analysis, Nucleic Acids Res., 2002 Mar 1, Vol. 30, No. 5 e21, 9 pp.	<input type="checkbox"/>
	14	GITAN, R. S. et al., "Methylation-Specific Oligonucleotide Microarray: A New Potential for High Throughput Methylation Analysis", Genome Res., 12, 2002, pp. 158-164.	<input type="checkbox"/>
	15	ROCKE, D. M. et al., "A Two-Component Model for Measurement Error in Analytical Chemistry", Technometrics May 1995, Vol. 37, No. 2, pp.176-184.	<input type="checkbox"/>
	16	DURBIN, B.P. et al., "A variance-stabilizing transformation for gene-expression microarray data", Bioinformatics, 18,1 , 2002, pp. S105-110.	<input type="checkbox"/>
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	21	www.Qiagen.com, Repli-g Mini/Midi Handbook, October 2005, 32 pages.	<input type="checkbox"/>
	22	ROCKE, D.M. et al., "A Model for Measurement Error for Gene Expression Arrays", Journal of Computational Biology, 2001, 8, no. 6, pp. 557-569.	<input type="checkbox"/>
	23	FRAGA, M.E. et al., "DNA Methylation: A Profile of Methods and Applications", Biotechniques 33, September 2002, pp. 632-649.	<input type="checkbox"/>
	24	FROMMER, M. et al. "A genomic sequencing protocol that yields a positive display of 5-methylcytosine residues in individual DNA strands", ProcNatl Acad Sci U S A, 1992 Mar 1, Vol. 89, No. 5, pp. 1827-31.	<input type="checkbox"/>
	25	OLEK, A. et al., "A modified and improved method for bisulphite based cytosine methylation analysis", Nucleic Acids Res, 1996 Dec 15, Vol. 24, No. 24, pp. 5064-5066.	<input type="checkbox"/>
	26	BRANSTEITTER, R. et al., "Activation-induced cytidine deaminase deaminates deoxycytidine on single-stranded DNA but requires the action of RNase", Proc Natl Acad Sci USA, Apr 1, 2003, Vol. 100, No. 7, pp. 4102-4107.	<input type="checkbox"/>
	27	WETMUR, J.G., "Hybridization and Renaturation Kinetics of Nucleic Acids", Annual Reviews, 1976, pp. 337-362.	<input type="checkbox"/>
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	29	Eads, C. A. et al., "Epigenetic Patterns in the Progression of Esophageal Adenocarcinoma", Cancer Research, 61, April 15, 2001, pp. 3410-3418.	<input type="checkbox"/>
	30	HEID, C.A. et al., "Real time quantitative PCR", Genome Res. 1996, Vol. 6, pp. 986-994.	<input type="checkbox"/>

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EXAMINER SIGNATURE

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